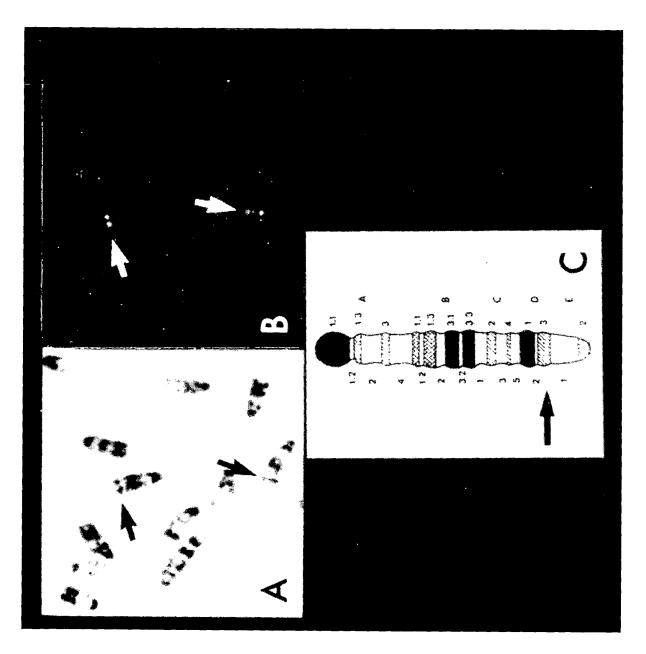
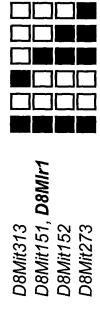


Figure 1



Jackson Chromosome 8



SE 1.64 0.75 0.91

R 5.32 1.06 1.59

Figure 3

ACC#	species human	exons represented 40	DNA homology 90%	library Soares_testis_
T47371	human	83	87%	Strgn. #937225
BF567477	rat	40	95%	UI-R-BO0
BE665278	bovine	84-87	83%	Marc 4bov
		78-79	82%	
BF077884	píg		83%	Marc 2pig
BF078559	pig	66-67	03%	Marc 2pig
BB573629	mouse	0.7	0001	adlt testis
AV278035	mouse	87	99%	adlt testis
BB015925	mouse	87	98%	adit testis
BB555992	mouse	87	94%	prg ovary
BF042472	bovine	81-83	86%	placenta
BE935732	human			nervous
AW880607	human	31-34	83%	adlt ovary
AW880545	human	31-33	84%	adit ovary
BE935729	human			nervous
BF361871	human	34-36	83%	nervous
BB664150	mouse	1 thru 5	99%	neonate lung
BB616892	mouse	75-78	98%	adult testis
BQ840375	mouse	87	100%	spermatocyte
BB641870	mouse	1and 3	98%	neonate cortex
BQ560006	mouse	20	100%	Mouse 7.4K
BB573629	mouse	47-48	96%	adult testis
BG771496	human	3 thru 7	85%	NIH_MGC_97
BF352620	human	5 thru 8	85%	HT0618
BG829246	human	55-59	81%	NIH_MGC_17
AU128584	human	3 thru 6	83%	NT2RP2
BF352665	human	4 thru 6 & 8	86%	HT0618
BF352642	human	5 thru 8 (additional)	86%	HT0618
AL556977	human	8 & 9	86%	LTI FL012 TC1
BG999183	human	51 & 52	85%	HT1311
BQ776506	human	24	86%	HR85 islet
BM725878	human	38-40	87%	UI-E-EJ0
BM677992	human	39-40	87%	UI-E-EJ0
W26351	human	15-18	82%	adult retina
BG005773	human	22-24	82%	GN0240
AW901070	human	6 thru 8	86%	NN1010
BG928962	human	70-73	80%	Norm. Cartilage
AL705531	human	3 thru 5	84%	hlcc3
AA431373	human	17-19	80%	Soares_testis
AW292266	human	87	0070	NCI_CGAP
AI809964	human	87	85%	mixed
Al693718	human	87	84%	mixed
A1693696	human	87	84%	mixed
Al564238	human	87	84%	NCI CGAP Ut1
AA488706	human	15-16	87%	Strgn. #937210
AI824393		87	84%	NCI_CGAP_Ut1
	human			
Al829538	human	87	84%	NCI_CGAP_Ut1
BF376220	human	4 thru 5	83%	TN0036
BQ448683	human	15 thru 16	86%	NCI_CGAP_Ct1
N50787	human	87	83%	2NbHMSP
BQ776830	human	19-24	83%	HR85 islet
AW896634	human	8 thru 9	85%	NN0050
BE549744	human	24	88%	NCI_CGAP_Lu24
Al689735	human	24	88%	NCI_CGAP_Lu24
BG992430	human	73-76		HT0999

	_	recented	DNA homology	library
ACC#	species	exons represented	79%	hlcc3
AL703616	human	48-51	93%	NN0044
BE935732	human	85	93%	NN0044
BE935729	human	85	83%	hlcc3
AL712790	human	7		NIH_MGC_97
BI560655	human	67-68	83%	HT0618
BQ352231	human	7 thru 8	90%	NN0009
AW893199		15	89%	
	human	80-81	84%	TN0136
BF093325		87	89%	UI-R-CA0
BF402637	rat	87	81%	MARC 2PIG
BF199199	pig	- -	89%	MARC 2PIG
BF199193	pig	87	30.11	

Human Hydin cDNA (SEQ ID NO: 14)

AGCTCGGGCGGCATGGAGAGTGCGGGCGGCTTCAAGCTGGGTATGGAGCCCCTCAGCGGC GGCGGGGTCTGTGAGTTGGACGCGGGGTCTTGGCGGGGAATGGAGGTAGAATAAACGTGGGA CCCGGAGTGCACCAAGGTGAGAAAAAAAATTACTAAAAATGACAAGTAGAAGACTTGAGGA GTCCATGGGGGCTGTTCAGATGGGATTGGTCAATATGTTCAAAGGATTTCAAAGCAAGGTTT TGCCACCCTGAGTCCAAAGGTGGTTACAGAAGAAGAAGTAAACCGAATGCTTACACCCTCA GAGTTCCTGAAGGAAATGTCCCTGACCACCGAGCAGAGACTGGCAAAAACACGTTTGATGTG CCGACCACAGATCATCGAACTCTTAGATATGGGGGAAACAACACATCAGAAGTTTTCAGGAA TTGACCTGGATCAGGCATTATTCCAGCCCTTTCCATCAGAAATTATATTTCAGAACTACACT CCCTGTGAAGTCTATGAAGTTCCACTGATTTTGAGGAACAATGACAAAATTCCAAGGTTGGT GAAAGTTGTGGAAGAAAGTTCGCCTTACTTTAAAGTAATCAGCCCCAAAGATATTGGCCACA AAGTGGCTCCTGGAGTGCCTTCCATATTCCGAATCCTCTTTACTCCAGAGGAGAACAAGGAT TACGCCCATACGTTGACCTGTGTTACTGAAAGAGAAAAGTTTATTGTACCCATCAAAGCTAG AGGGGCACGAGCCATTCTCGATTTTCCTGACAAGCTGAATTTTTCCACTTGTCCTGTCAAAT ACAGCACCAGAAGATTCTGCTGGTACGAAACATTGGCAACAAAAATGCTGTATTTCACATC AAAACTTGTAGGCCTTTCTCTATAGAACCAGCTATTGGAACTCTTAATGTGGGAGAGTCCAT GCAACTGGAAGTGGAGTTTGAGCCACAGAGTGTGGGCGATCACAGTGGAAGACTTATCGTGT GTTATGACACAGGTGAAAAGGTGTTTGTATCTCTCTATGGAGCTGCCATAGACATGAATATA AGGCTGGATAAGAATTCCTTGACCATCGAGAAAACCTACATATCTCTGGCCAATCAGCGAAC TATAACCATTCACAATCGCAGTAATATCATTGCCCATTTCCTGTGGAAGGTATTTGCTACCC AGCAAGAAGAGACAGAGAAAAATATAGGGCCTGTGATGATCTGATCAAAGAGGAGAAGGAT GAGACTGATGAGTTTTTTGAAGAGTGCATTACTGATCCTTTACTCCGAGAACATCTTTCTGT TCTGTCCCGAACCTTTGCGAATCAAAGGAGGCTGGTGCAGGGAGACAGCAAACTGTTCTTCA ATAACGTTTTCACTGTGGAGCCCCTGGAAGGTGATGTCTGGCCCAACTCATCAGCTGAAATC ACCGTGTACTTTAACCCACTAGAAGCCAAGCTCTATCAACAGACCATTTACTGCGACATTTT AGGCCGAGAAATCCGTCTGCCCCTCCGAATCAAAGGGGAAGGCATGGGACCTAAGATTCACT TCAACTTTGAATTGCTGGATATTGGGAAAGTTTTCACTGGATCTGCACATTGTTATGAGGCG ATACTGTACAACAAGACAGCATCGATGCTCTCTTCAACATGACCCCTCCAACTTCAGCTTT GGGGGCCTGCTTTGTTTTCAGTCCCAAGGAAGGCATCATTGAACCAAGTGGAGTCCAAGCTA TCCAGATCTCCTTCAGCTCTACCATCCTGGGAAACTTTGAAGAAGAGTTCCTGGTCAATGTC TTTTAATGTTCCAGCTCTGCACTTTGGTGATGTTTCCTTTGGGTTTCCTCATACCTTGATAT GTTCCCTCAATAATACCTCTTTGATCCCCATGACTTACAAACTGCGTATCCCTGGGGATGGC CTTGGCCATAAAAGCATTTCATATTGTGAGCAGCATGTGGACTACAAAAGACCGTCTTGGAC CAAGGAAGAAATATCCTCAATGAAACCAAAAGAATTCACCATCTCTCCTGACTGTGGCACCA TTCGCCCCCAGGGATTTGCTGCTATCAGGGTGACATTATGCTCCAACACTGTACAGAAATAC GAGCTGGCACTCGTGGTGGACGTGGAGGGCATCGGAGAAGAGGTGCTGGCGCTCTTAATTGC AGCAAGGTGTGTTGTACCTGCCCTCCACCTGGTCAATACAGAGGTGGACTTTGGGCACTGCT TCCTGAAGTACCCGTATGAGAAAACACTCCAGCTTGCCGATCAAGATGACCTCCCAGGATTC TATGAGGTCCAGCCTCAGGTGTGTGAGGAGGTGCCTACTGTGCTGTTTTCCAGCCCCACCCC CAGCGGGGTCATCTCCCCAAGCAGCACCATCCACATACCACTGGTCCTGGAGACCCAGGTCA CTGGAGAACACAGATCCACGGTTTACATCTCAATCTTTGGGAGCCAGGACCCCCCTTTGGTA TGTCACTTAAAGAGCGCTGGAGAAGGCCCAGTTATCTACGTCCATCCCAATCAAGTGGACTT CGGGAATATCTACGTCCTAAAAGACTCTTCCAGGATTCTCAACCTATGCAACCAGTCCTTCA TTCCCGCATTTTTCCAGGCACACATGGCACACAAAAAATCCCTTTGGACGATTGAACCCAAT GAAGGCATGGTTCCTCCAGAAACTGATGTTCAACTGGCACTGACCGCCAACCTGAATGACAC ACTGACATTCAAGGACTGTGTTATTTTGGACATTGAAAATAGCAGTACCTATCGGATTCCTG TTCAGGCTTCCGGAACTGGTTCCACTATTGTTTCAGATAAGCCCTTTGCTCCAGAACTCAAT TTGGGGGCACATTTTAGCCTGGATACCCACTATTACCACTTTAAGTTGATCAACAAGGGACG TCGGATCCAACAGTTGTTCTGGATGAATGATAGCTTCCGACCCCAGGCCAAGCTGAGTAAGA AGGGCCGGGTTAAGAAGGGACATGCTCATGTCCAACCCCAGCCCAGTGGCTCTCAGGAGCCC AGGGATCCACAGAGCCCCGTGTTTCATCTCCACCCCGCCAGCATGGAGCTGTACCCAGGCCA GGCAATTGATGTGATACTCGAAGGCTATTCTGCTACTCCCAGGATAGTGAAAGAGAAGCTGG TGTGCCACGCCATCATCGGGGCACAGAAGGGGAAGAGCTTGGTGATGGCTGTGAACATCACC TGTGAGTTCGTCGCACCTCTCATCCAGCTCTCCACCAAGCAGCTCATCTACCGACTGGAGAA GAAACCTAACAGTATCCTGAAACCTGATTACCAGCCCTTGGCCGTAAAGAACATTTCCACCC TGCCCGTGAACTTGTTGCTGTCAACATCTGGACCCTTCTTTATATGTGAGACTGATAAATCC CTGCTGCCGGCAACTCCTGAGCCTATTAAACTGGAAATTGATGAAGAAAAAAACCTGCTGAT CAAGTTTGACCCTTCCTACAGAAACGATCTGAACAACTGGGTGGCAGAAGAAATTCTAGCAA TTAAGTATGTGGAACACCCTCAGATAGACAGCCTGGACCTGCGCGGAGAAGTGCATTACCCC AACCTCAGCTTTGAGACAAAGGAGCTGGATTTTGGCTGCATCCTGAACGATACTGAGCTCAT TCGCTACGTTACCATCACCAACTGCAGTCCGTTGGTTGTGAAGTTTCGCTGGTTCTTCTTGG TGAATGATGAGGAAAATCAGATAAGGTTTGTGACATTGCCAAAGAAGCCCTACAGTGCCCCA CTGTCCCAGATGGAGTCCATCCCAGCAACCTCAGAGGCTGCCAGCCCACCAGCAATCCTAGT TACAGTAGAGTCCCCCGAGATGGATTTAAATGATTTTGTTAAGACTGTCCTTGTGGATGAAG ATGCCAGGCCTGAAGAAAAGAACTAAGAAAAACAAAAGCTTCCAGTGTGATCTCAGATGAA ATAAAAATTAGCTCTACTGAAATAGAAAGAATATACTCAAGCCAGAGCCAGGTGGAGGATCA GGAATCCCTACAGACCTGTGAACAGAATGAGATGCTTTCCATTGGGATAGAAGAAGTGTTTG ATATTTTGCCCCTGTTTGGAGTGTTGCAGCCACACAGTAGCCACCAAATATCGTTCACCTTC TATGGACACGCTAACATCATTGCACAAGCTAAAGCTCTGTGTGAAGTGGAAGAAGGACCCAC CTACGAAATAACACTGAAGGGAGAGGCGTCCCTGGTCAACTATTCCTTTGACACCAAGGATA TTCACTACGGATTACAGCTGTTTGACCATGTCACAGAGAGGGAAATCACGCTGACGAACATG GGGAAAGTTGGCTTTGAGTTCAAGGTTCTGACTGACCACCAGTCTTCTCCAGACAACCTTCT CCCTGGAGTGCCACTAATCCTGCCTGTGTCTGGCTTTATCAGTTCACATCAAGAGCAGGTAT TAAAAGTTTACTACCTACCTGGAGTACCTGAGGTCTTTAAAAGGAGTTTCCAGATACAGATC GCCCACCTGGACCCAGAAAATATCACTCTGAGCGGAGAGGGAATCTTTCCCCAAATCTGCCT CGATCTCCCCAGGAACCTCACAGCAAATGAAAAGTATGAAATGTTCTTGAATCAAGCCAGGA 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CCGAGGCACGTTCTCATTTGAATTTCAGCCCCTGAAAGCTGGAGAAACCTTCGGAAGACTA ACTTTGCACAACACTGACTTGGGTTACTACCAATATGAGCTCTATCTGAAAGCCACGCCAGC ACTTCCGGAAAAGCCTGTTCACTTCCAGACTGTCCTTGGCAGCCGAAATCATCCTTGTGA AGTTCATCAATTACACACGGCAGAGGACAGAATACTACTGCAGGACCGACTGTACAGACTTC CACGCAGAAAAACTCATTAATGCAGCCCCAGGAGGCCAGGGAGGCACTGAAGCCAGTGTGGA AGTCTTATTCGAGCCAGCCACCTGGGTGAGACCAAGGGCATCCTGATCCTATCATCGCTCG CAGGTGGAGAGTATATCATCCCCCTCTTTGGAATGGCTCTGCCTCCCAAGCCCCAAGGTCCC TTCTCGATCCGAGCCGGGTACAGCATAATCATCCCCTTCAAGAATGTCTTCTATCACATGGT GACCTTCTCCATCATCGTGGATAACCCAGCCTTCACCATTCGCGCTGGAGAGTCTGTGCGGC CCAAGAAGATCAACACCACAGTCTCCTTTGAAGGAAACCCATCTGGCAGCAAAACCCCC ATCACCACCAAGCTGACTGTGAGCTGCCCTCCTGGTGAAGGGAGTGAGACTGGAGTTAAATG GGTTTATTATCTGAAGGGGATCACCCTTTAGTGGTAACCAGGGTTACCTGTATCAACCAAAA GCTATGCATTGTCTTAGCCTGAAAAAGAATAGAGAAAACAATAAGAATTCTAAAGGAACTGT TTTTATTCTTCTCATACAATTATAGGGCAGTTATTTCCCTATTATGTGTTTTCCAAATATAG ATATGAAATATCTATTCCATATTAAACATTATAACTACACACAA

Human Hydin Protein(SEQ ID NO:15)

 ${\tt MGAVQMGLVNMFKGFQSKVLPPLSPKVVTEEEVNRMLTPSEFLKEMSLTTEQRLAKTRLMCR}$ PQIIELLDMGETTHQKFSGIDLDQALFQPFPSEIIFQNYTPCEVYEVPLILRNNDKIPRLVK VVEESSPYFKVISPKDIGHKVAPGVPSIFRILFTPEENKDYAHTLTCVTEREKFIVPIKARG ARAILDFPDKLNFSTCPVKYSTQKILLVRNIGNKNAVFHIKTCRPFSIEPAIGTLNVGESMQ LEVEFEPOSVGDHSGRLIVCYDTGEKVFVSLYGAAIDMNIRLDKNSLTIEKTYISLANQRTI TIHNRSNIIAHFLWKVFATQQEEDREKYRACDDLIKEEKDETDEFFEECITDPLLREHLSVL SRTFANORRLVOGDSKLFFNNVFTVEPLEGDVWPNSSAEITVYFNPLEAKLYQQTIYCDILG REIRLPLRIKGEGMGPKIHFNFELLDIGKVFTGSAHCYEAILYNKDSIDALFNMTPPTSALG ACFVFSPKEGIIEPSGVQAIQISFSSTILGNFEEEFLVNVNGSPEPVKLTIRGCVIGPTFHF NVPALHFGDVSFGFPHTLICSLNNTSLIPMTYKLRIPGDGLGHKSISYCEQHVDYKRPSWTK EEISSMKPKEFTISPDCGTIRPOGFAAIRVTLCSNTVOKYELALVVDVEGIGEEVLALLIAA RCVVPALHLVNTEVDFGHCFLKYPYEKTLQLADQDDLPGFYEVQPQVCEEVPTVLFSSPTPS GVISPSSTIHIPLVLETQVTGEHRSTVYISIFGSQDPPLVCHLKSAGEGPVIYVHPNQVDFG NIYVLKDSSRILNLCNQSFIPAFFQAHMAHKKSLWTIEPNEGMVPPETDVQLALTANLNDTL TFKDCVILDIENSSTYRIPVQASGTGSTIVSDKPFAPELNLGAHFSLDTHYYHFKLINKGRR IQQLFWMNDSFRPQAKLSKKGRVKKGHAHVQPQPSGSQEPRDPQSPVFHLHPASMELYPGQA IDVILEGYSATPRIVKEKLVCHAIIGAQKGKSLVMAVNITCEFVAPLIQLSTKQLIYRLEKK PNSILKPDYQPLAVKNISTLPVNLLLSTSGPFFICETDKSLLPATPEPIKLEIDEEKNLLIK FDPSYRNDLNNWVAEEILAIKYVEHPQIDSLDLRGEVHYPNLSFETKELDFGCILNDTELIR YVTITNCSPLVVKFRWFFLVNDEENQIRFVTLPKKPYSAPLSQMESIPATSEAASPPAILVT VESPEMDLNDFVKTVLVDEDARPEEKELRKTKASSVISDEIKISSTEIERIYSSQSQVEDQE SLOTCEONEMLSIGIEEVFDILPLFGVLQPHSSHQISFTFYGHANIIAQAKALCEVEEGPTY EITLKGEASLVNYSFDTKDIHYGLOLFDHVTEREITLTNMGKVGFEFKVLTDHQSSPDNLLP GVPLILPVSGFISSHQEQVLKVYYLPGVPEVFKRSFQIQIAHLDPENITLSGEGIFPQICLD LPRNLTANEKYEMFLNQARKNTDKEYNKCEMLDHFDVITEEVPEDEPAEVSAHLQMEVERLI VOSYVLEHOKTTTPDPMDDPCFSHRSRRKLAKIQLPEYILDFGYIILGEVRTHIIKIINTSH FPVSFHADKRVLHETGFSTELDRVKNLPHCETEIFEVRFDPOGANLPVGSKEVILPIKVVGG PTVHICLQAKVTIPTMTLSRGKVDFATIQCGQCLVETIQLSNHLQVPCEWFVQSQKPVDKLE KHMPKYLRQKLRAELKPKTRIFEIQPISGVLDPGEKSNVQVKFMPKEEKFYSQTLVFQIAQS AOKLTLLARGOGLEPRLEFSPSVLDLGPLLLCAPGDEAEVIVKNPCNFPIEFYSLEFDQQYL IEEKILRKLKGYDSYNTLLLPPHNPGEKLPPELYEYFKEIKKSKEEOMRAKYLENLAQEN EEEDITSSDQGTSNSTKRTSLSRGISVTSNLEEWHALLVESKTYLEEEEDEESLEKIIFQTD KLQSIDSHSMEEVGEVENNPVSKAIARHLGIDISAEGRLAKNRKGIAIIIHGTPLSGKSANA VSVAKYYNAACLSIDSIVLEAVANSNNIPGIRACELCIRAAIEQSMKEGEEAAQEAAVGQNV IGOGRLSTDTLGKLASEMTLVAPEIKPGKSVRGSVVITKSKADSHGSGSQKQHHSHQSETPQ ISSSPLPPGPIHRWLSVSPSVGGETGLMSCVLPDELLVQILAERIQLSDCYRGVVFDGLDTL FARNAAAALLCLLKAIGSREHIYILNMAQDYAAMKAREKAKKEQEERKHKGALEKEKERLQN MDEEEYDALTEEEKLTFDRGIQQALRERKKREQERLAKEMQEKKLQQELERQKEEDELKRRV KKGKOGPIKEEPPMKKSQAANKQVPPLTKVDVKMETIERKISVREQTMSEKEELNKKKRNMG DVSMHGLPLVQDQEDSEGDNSKDPDKQLAPKFKTYELTLKDVQNILMYWDRKQGVQLPPAGM $\verb"EEAPHEPDDQRQVPLGGRRGRKDRERERLEKERTEKERLEREKAERERLEKLRALEERSDWE"$ GEGEEDHEGKKEKDLGVPFLDIQTPDFEGLSWKQALESDKLPKGEQILDILGLGASGPPIPP PALFSIVSYPVKRPPLTMTDDLEHFVFVIPPSEDISLDEKKEMEIESDFLATTNTTKAOEEO TSSSKGGKQKMKEKIDQVFEIQKDKRHMALNRKVLSGEPAGTISQLSDTDLDNFNGQHSQEK FTRLNHFRWIVPANGEVTLQVHFSSDEFGNFDQTFNFEILGTCCQYQLYCRGICTYPYICQD 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CKLSRIMFOLPADOVPDWDDRMHTVKWVDVPRNMPGTFTTKRKVIETDPEPAHSVLEENYOE LQLQISANVDFASYHCQARDVRFKETLVYQTRVFEFDVINSGRVQLEFSWVSEDTSKAVSFA KPDHQGSAQKDQLSQGTMHTGSTLDSTMDHWAEGSPQPFSVEPSSGIVPVGKIQKFKVKFSP LDIGDFESNLFCOIPNLPPGEOGPVLVAKGRSTLPICHFDLKDSDYISGHORNPELRGSSGG ALDPNTRVIEFTTVGIGGKNLRTFTILNPTNSTYSFCWISEIVFOFTPFHLGITESSWTFLI PEHNITIVFQFTPFHLGITESSWTFLIPEHNITVPFLLVGKTTEPLISLNKSHLNFSSLLIG REARETVQIINKEEQGFDFSFQDNSRYSEGFSNSLLVCPMEGWIPPLSRFPIDIFFTPKQEG DVNFNLICNVEKKVHPVTLNVKAEGYTMNVEIKCKDRTGSITLLTPNOTNIINFYEVELNEC VQCEFNFINTGKFTFSFQAQLCGSKTLLQYLEFSPIDSTVDVGQSVHATLSFQPLKKCVLTD LELIIKISHGPTFMCNISGCAVSPAIHFSFTSYNFGTCFIYQAGMPPYKQTLVITNKEETPM SIDCLYTNTTHLEVNSRVDVVKPGNTLEIPITFYPRESINYQELIPFEINGLSQQTVEIKGK GTKMKILVLDPANRIVKLGAVLPGOVVKRTVSIMNNSLAOLTFNOSILFTIPELOEPKVLTL APFHNITLKPKEVCKLEVIFAPKKRVPPFSEEVFMECMGLLRPLFLLSGCCOALEISLDOEH IPFGPVVYQTQATRRILMMNTGDVGARFKWDIKKFEPHFSISPEEGYITSGMEVSFEVTYHP TEVGKESLCKNILCYIOGGSPLSLTLSGVCVGPPAVKEVVNFTCOVRSKHTOTILLSNRTNO TWNLHPIFEGEHWEGPEFITLEAHOONKPYEITYRPRTMNLENRKHOGTLFFPLPDGTGWLY ALHGTSELPKAVANIYREVPCKTPYTELLPITNWLNKPQRFRVIVEILKPEKPDLSITMKGL DYIDVLSGSKKDYKLNFFSHKEGTYAAKVIFRNEVTNEFLYYNVSFRVIPSGIIKTIEMVTP VROVASASIKLENPLPYSVTFSTECRMPDIALPSOFVVPANSEGTFSFEFOPLKAGETFGRL TLHNTDLGYYQYELYLKATPALPEKPVHFQTVLGSSQIILVKFINYTRQRTEYYCRTDCTDF HAEKLINAAPGGQGGTEASVEVLFEPSHLGETKGILILSSLAGGEYIIPLFGMALPPKPQGP FSIRAGYSIIIPFKNVFYHMVTFSIIVDNPAFTIRAGESVRPKKINNITVSFEGNPSGSKTP ITTKLTVSCPPGEGSETGVKWVYYLKGITL

Murine Hydin cDNA(SEQ ID NO:16)

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